

## Sequence Comparison A

### RESULT 1

US-09-383-586-31

; Sequence 31, Application US/09383586

; Patent No. 6242419

; GENERAL INFORMATION:

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Abernethy, Nevin

; APPLICANT: Onrust, Rene

; APPLICANT: Kumble, Anand

; APPLICANT: Murison, Greg

; TITLE OF INVENTION: Compounds isolated from stromal cells

; TITLE OF INVENTION: and methods for their use

; FILE REFERENCE: 11000.1037c1

; CURRENT APPLICATION NUMBER: US/09/383,586

; CURRENT FILING DATE: 1999-08-26

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 31

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Mouse

US-09-383-586-31

Query Match 85.2%; Score 2308.5; DB 3; Length 529;  
Best Local Similarity 88.0%; Pred. No. 4.7e-181;  
Matches 431; Conservative 22; Mismatches 26; Indels 11; Gaps 2;

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Qy      1 MTPSPLLLLLLLPPLLLGAFPPAAAARGPPKMAKVVPRQVARLGRTVRLQCPVEGDPPPL 60
      || || ||| ||||| | | |||||:||||||| ||||| ||||| |||||
Db      1 MTRSPALLL----LLLGALPSAEAAARGPPRMADKVVPRQVARLGRTVRLQCPVEGDPPPL 56

Qy     61 TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     57 TMWTKDGRTIHSGWSRFRVLPQGLKVKVEAEDAGVYVCKATNGFGSLSVNYTLIIMDDI 116

Qy    121 SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 180
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    117 SPGKESPGPGSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 176

Qy    181 DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240
      || ||||| || |||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    177 DIMWMKDDQTLTHLEASEHRKKKWTLSLKNLKPEDSGKYTCRVSNKAGAINATYKVDVIQ 236

Qy    241 RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGAEGRHNSTIDVGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    237 RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGSEGRHNSTIDVGG 296

Qy    301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    297 QKFVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK 356

Qy    361 PPGPPVASSSSATSLFPWPVVIGIPAGAVFILGTLLLWLCAQKKPCTPAPAPPLPGHRPP 420
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    357 PPGPPMASSSSSTSLFPWPVVIGIPAGAVFILGTVLLWLCAQKKKPCAPASTLPVPGHRPP 416

Qy    421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHT 480
      ||:|:||||||| ||||| ||||| |||||:| | ||||| |||||:|
Db    417 GTSRERSGDKDLPSLA-----VGICEEHGSAMAPQHILASGSTAGPKLYPKLYTDVHT 469

Qy    481 HTHTHSHTHS 490
      |||||: ||:
Db    470 HTHTHCTHT 479
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## Sequence Comparison B

RESULT 2

Q9H4D7

ID Q9H4D7 PRELIMINARY; PRT; 504 AA.  
 AC Q9H4D7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE FGFR-like protein precursor (Fibroblast growth factor receptor  
 DE 5).  
 GN FGFR1 OR FGFR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cartilage;  
 RX PubMed=11031111;  
 RA Wiedemann M., Trueb B.;  
 RT "Characterization of a novel protein (FGFR1) from human cartilage  
 RT related to FGF receptors.";  
 RL Genomics 69:275-279(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21167383; PubMed=11267671;  
 RA Kim I., Moon S.O., Yu K.H., Kim U.H., Koh G.Y.;  
 RT "A novel fibroblast growth factor receptor-5 preferentially expressed  
 RT in the pancreas.";  
 RL Biochim. Biophys. Acta 1518:152-156(2001).  
 DR EMBL; AJ277437; CAC14171.1; -.  
 DR EMBL; AF279689; AAK26742.1; -.  
 DR GO; GO:0016021; C:integral to membrane; NAS.  
 DR GO; GO:0005007; F:fibroblast growth factor receptor activity; NAS.  
 DR GO; GO:0001558; P:regulation of cell growth; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00408; IGc2; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 KW Immunoglobulin domain; Receptor; Signal.  
 FT SIGNAL 1 17 POTENTIAL.  
 SQ SEQUENCE 504 AA; 54567 MW; 16382E57D4276485 CRC64;

Query Match 99.7%; Score 2701; DB 4; Length 504;  
 Best Local Similarity 99.8%; Pred. No. 9.3e-206;  
 Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTPSPLLLLLLPPLLGAFPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPL	60
Db	1	MTPSPLLLLLLPPLLGAFPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPL	60
Qy	61	TMWTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Db	61	TMWTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Qy	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP	180
Db	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP	180
Qy	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Db	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Qy	241	RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSVDPKPIQWLKRVEYGAEGRHNSTIDVGG	300
Db	241	RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSVDPKPIQWLKRVEYGAEGRHNSTIDVGG	300
Qy	301	QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK	360

Db	301	QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPK	360
Qy	361	PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP	420
Db	361	PQGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP	420
Qy	421	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT	480
Db	421	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT	480
Qy	481	HTHTSHTHSHVEGKVHQHIHYQC	504
Db	481	HTHTSHTHSHVEGKVHQHIHYQC	504